



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 137-313

**TO: Patricia Duffy**  
**Location: REM/3B05/3C18**  
**Art Unit: 1645**  
**Monday, November 15, 2004**  
**Case Serial Number: 09/765271**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**REM-1A65**  
**Phone: (571)272-2527**  
  
**paul.schulwitz@uspto.gov**

### Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2527

*Allie*

STIC-Biotech/ChemLib

159505

From: Duffy, Patricia  
Sent: Tuesday, November 09, 2004 3:48 PM  
To: STIC-Biotech/ChemLib  
Subject: Quick comparison search of proteins.  
  
Importance: High

IN re:09/765,271

Please run a comparison sequence search comparing SEQ ID NO:56 of 09/765,271 with Accession Number P91742 of SPTREMBL. I need the full length of p19742 compared. I am looking for a short region that has 8 consecutive amino acids in common with SEQ ID NO:56.

Thank you.

Patricia A. Duffy, Ph.D.  
Art Unit 1645, Remsen 3B05  
571-272-0855

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 11/15  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

GenCore

OM Protein - protein search, using sw model  
 Run on: November 15, 2004, 16:56:34 ; Search time 0.001 Seconds  
 (without alignments)  
 1.22.584 Million cell updates/sec  
 Title: us-09-765-271-56  
 Perfect score: 4165  
 Sequence: 1 SYELGIYQARTVKENNRSVY.....KLLALIKGSNPNSSVSKEKIN 796  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 1 seqs, 154 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : p91742.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.5	1.3	154	1 p91742	TOIG of: p91742

#### ALIGNMENTS

RESULT	1	p91742	TOIG of: p91742	check: 1859	from: 1 to: 154	RC	SEQUENCE FROM N.A.
						RX	Medline=97327060; PubMed=9183847;
						RA	Robertson H.M.;
						RT	"Multiple Mariner transposons in flatworms and hydroids are related to those of insects";
						RL	J. Hered. 88:195-201 (1997).
						DR	InterPro: IPR001888; Transposase_1.
						DR	PFam: PF01359; Transposase_1.
						FT	NON_TER 1 1
						FT	NON_TER 154 154